

FIG. 1

SEQ I.D. NO: 1:

2/10

AGTGGCCTGA TCGCGATGGG GACAAAGGCG CAAGTCGAGA GGAAACTGTT GTGCCTCTTC ATATTGGCGA 70

SEQ I.D. NO: 3: M G T K A Q V E R K L L C L F I L A I 19

TCCTGTTGTG CTCCCTGGCA TTGGGCAGTG TTACAGTGCA CTCTTCTGAA CCTGAAGTCA GAATTCCTGA 140

L L C S L A L G S V T V H S S E P E V R I P E 42

GAATAATCCT GTGAAGTTGT CCTGTGCCTA CTCGGGCTTT TCTTCTCCCC GTGTGGAGTG GAAGTTTGAC 210

N N P V K L S C A Y S G F S S P R V E W K F D 65

CAAGGAGACA CCACCAGACT CGTTTGCTAT AATAACAAGA TCACAGCTTC CTATGAGGAC CGGGTGACCT 280

O G D T T R L V C Y N N K I T A S Y E D R V T F 89

TCTTGCCAAC TGGTATCACC TTCAAGTCCG TGACACGGGA AGACACTGGG ACATACACTT GTATGGTCTC 350

L P T G I T F K S V T R E D T G T Y T C M V S 112

TGAGGAAGGC GGCAACAGCT ATGGGGAGGT CAAGGTCAAG CTCATCGTGC TTGTGCCTCC ATCCAAGCCT 420

E E G G N S Y G E V K V K L I V L V P P S K P 135

ACAGTTAACA TCCCCTCCTC TGCCACCATT GGGAAACGGG CAGTGCTGAC ATGCTCAGAA CAAGATGGTT 490

T V N I P S S A T I G N R A V L T C S E Q D G S 159

CCCCACCTTC TGAATACACC TGGTTCAAAG ATGGGATAGT GATGCCTACG AATCCCCAAA GCACCCGTGC 560

P P S E Y T W F K D G I V M P T N P K S T R A 182

CTTCAGCAAC TCTTCTATG TCCTGAATCC CACAACAGGA GAGCTGGTCT TTGATCCCCT GTCAGCCTCT 630

F S N S S Y V L N P T T G E L V F D P L S A S 205

GATACTGGAG AATACAGCTG TGAGGCACGG AATGGGTATG GGACACCCAT GACTTCAAAT GCTGTGCGCA 700

D T G E Y S C E A R N G Y G T P M T S N A V R M 229

TGGAAGCTGT GGAGCGGAAT GTGGGGGTCA TCGTGGCAGC CGTCCTTGTA ACCCTGATTC TCCTGGGAAT 770

E A V E R N V G V I V A A V L V T L I L L G I 252

CTTGTTT TTTT GGCATCTGGT TTGCCTATAG CCGAGGCCAC TTTGACAGAA CAAAGAAAGG GACTTCGAGT 840

L V F G I W F A Y S R G H F D R T K K G T S S 275

AAGAAGGTGA TTTACAGCCA GCCTAGTGCC CGAAGTGAAG GAGAATTCAA ACAGACCTCG TCATTCTCTGG 910

K K V I Y S Q P S A R S E G E F K Q T S S F L V 299

TGTGAGCCTG GTCGGCTCAC CGCCTATCAT CTGCATTGTC CTTACTCAGG TGCTACCGGA CTCTGGCCCC 980

TGATGTCTGT AGTTTCACAG GATGCCTTAT TTGTCTTCTA CACCCACAG GGGCCCTAC TTCTTCGGAT 1050

GTGTTTTTAA TAATGTCAGC TATGTGCCCC ATCCTCCTTC ATGCCCTCCC TCCCTTTCCT ACCACTGCTG 1120

AGTGGCCTGG AACTTGTTTA AAGTGTTTAT TCCTCATTTT TTTGAGGGAT CAGGAAGGAA TCCTGGGTAT 1190

GCCATTGACT TCCCTTCTAA GTAGACAGCA AAAATGGCGG GGGTCGCAGG AATCTGCACT CAACTGCCCA 1260

CCTGGCTGGC AGGGATCTTT GAATAGGTAT CTTGAGCTTG GTTCTGGGCT CTTTCCTTGT GTACTGACGA 1330

CCAGGGCCAG CTGTTCTAGA GCGGGAATTA GAGGCTAGAG CGGCTGAAAT GGTGTTTGG TGATGACACT 1400

GGGGTCTTTC CATCTCTGGG GCCCACTCTC TTCTGTCTTC CCATGGGAAG TGCCACTGGG ATCCCTCTGC 1470

CCTGTCTCTC TGAATACAAG CTGACTGACA TTGACTGTGT CTGTGGAAAA TGGGAGCTCT TGTTGTGGAG 1540

AGCATAGTAA ATTTTCAGAG AACTTGAAGC CAAAAGGATT TAAAACCGCT GCTCTAAGA AAAGAAAAC 1610

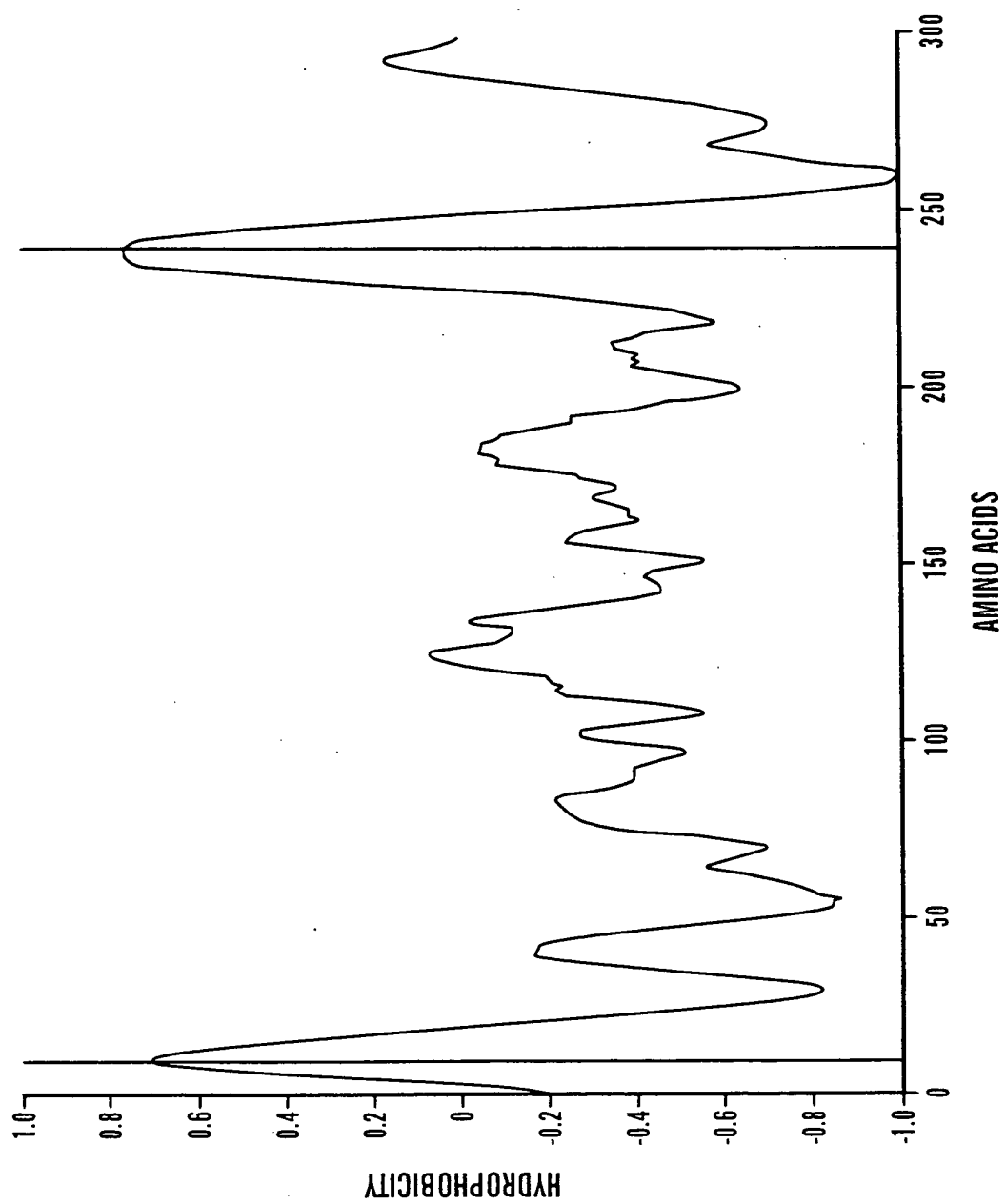
GGAGGCTGGG CGCAGTGGCT CACGCCTATA ATCCCAGAGG CTGAGGCAGG CGGATCACCT GAGGTCAGGA 1680

GTTCAGGATC AGCCTGACCA ACATGGAGAA ACCCTGCTGG AAATACAAAG TTAGCCAGGC ATGGTGGTGC 1750

ATGCCTGTAG TCCCAGCTGC TCAGGAGCCT GGCAACAAGA GCAAACTCC AGCTCAAAAA AAAAAAAAAA 1820

AA 1822

FIG. 2

**FIG. 3**

1. Amino acids 41-116 (25% identity to C2 profile)

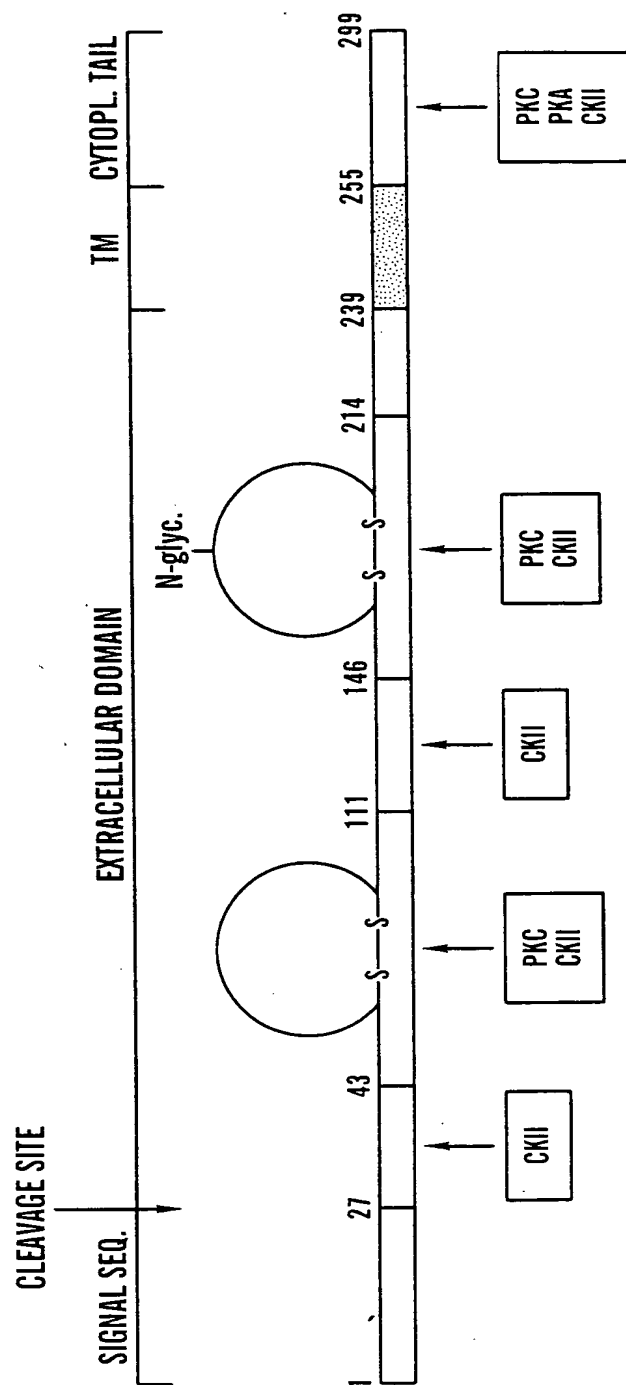
	---b---	---c---	---d---	---e---	---f---	
profile	LEGQSVTLT	PaagDPVPNITWLKdgkPLPe...	srlvaSGSTLTIKNVS	LED	SGLYTQVARN
41-116	PENNPVKLS	QAYSGFSSPRVENKF	DQDTRRLVCYNNKIT	ASYEDRVTFELPT	GITFKSV	TREDTGTYTQMVSEEGG
						SEQ I.D. NO: 8
						SEQ I.D. NO: 9

FIG. 4A

2. Amino acids 144-219 (30% identity to C2 profile)

	---b---	---c---	---d---	---e---	---f---	
profile	LEGQSVTLT	Pa.sgdPVPNITWLKd	gkPLPe.....s	rlvaSGSTLTIKNVS	LED	SGLYTQVARN
144-219	TIGNRAVL	TQSEQDGSPPSEY	TWFKDGI	VMPTNPKSTRAFSN	SYVLNPTTGELV	FDPLSASDTGEYSCEARN
						SEQ I.D. NO: 10
						SEQ I.D. NO: 11

FIG. 4B

**FIG. 5**

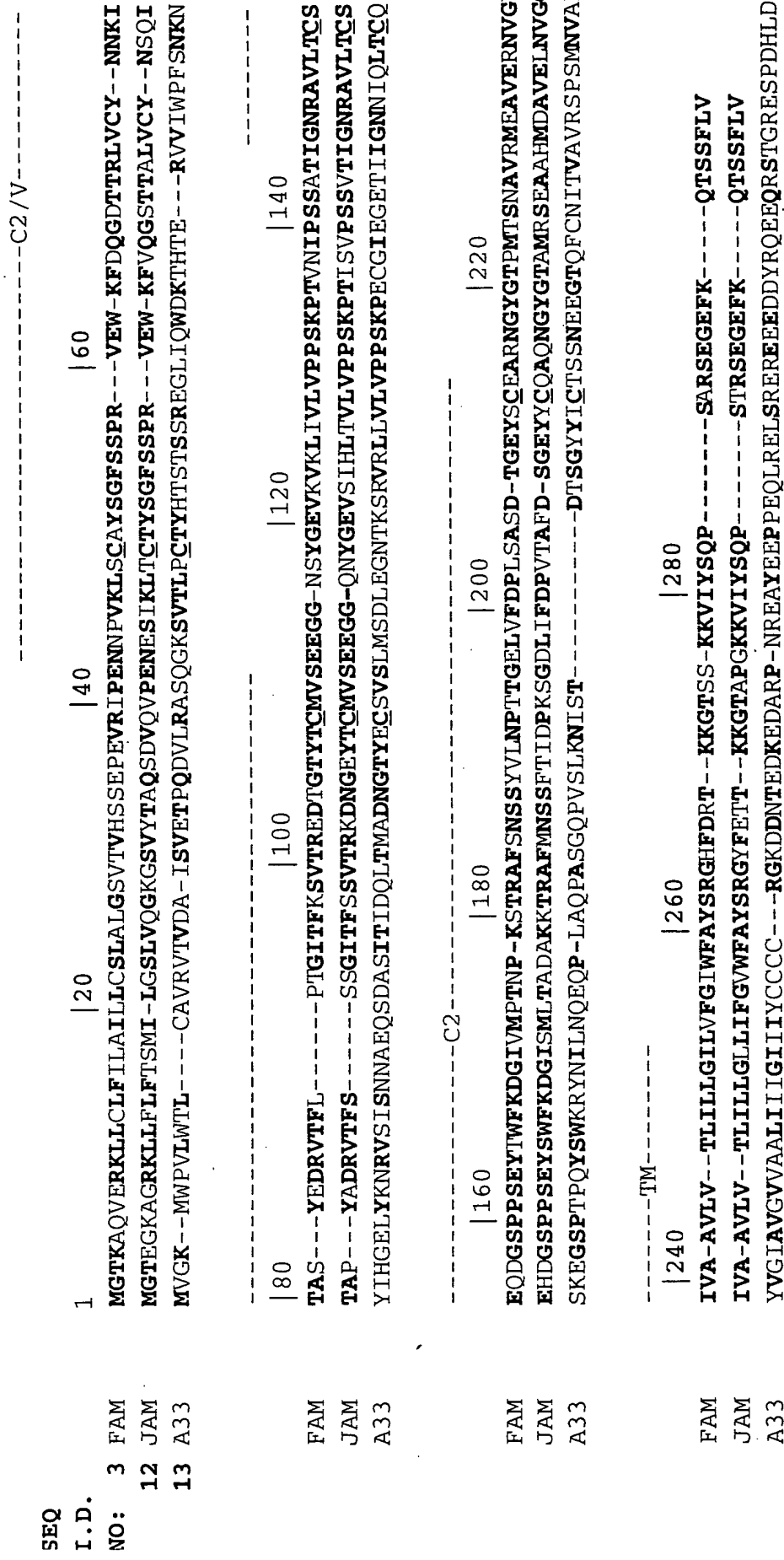


FIG. 6

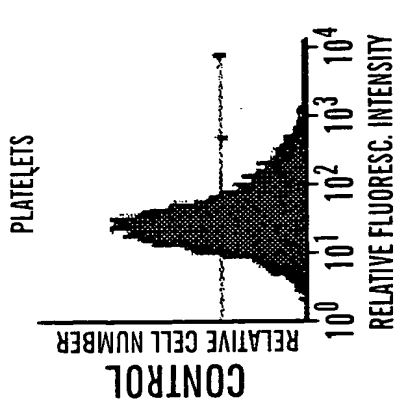
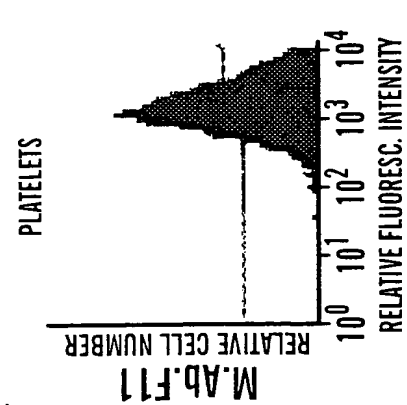


FIG. 7A

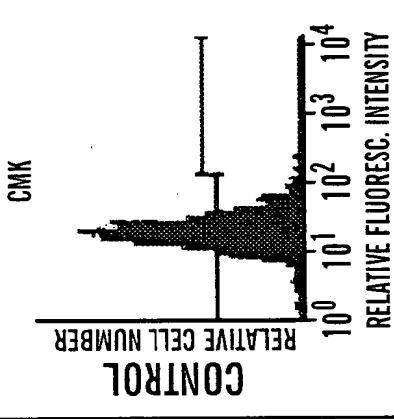
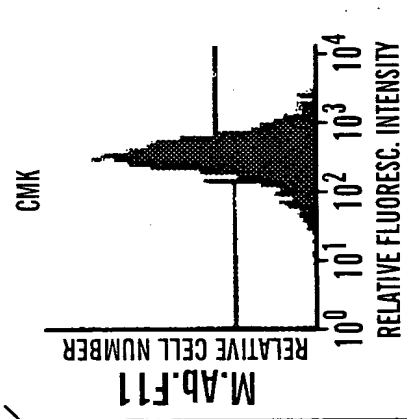


FIG. 7B

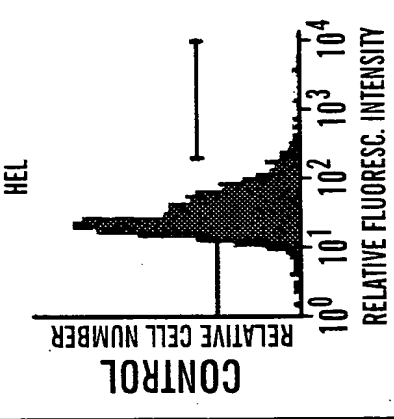
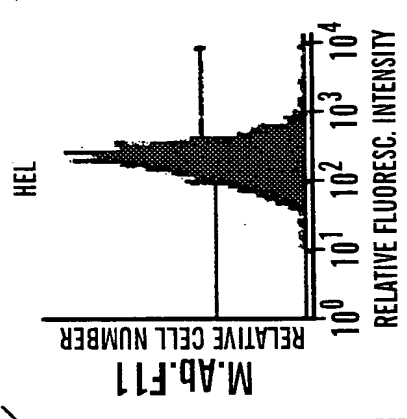


FIG. 7C

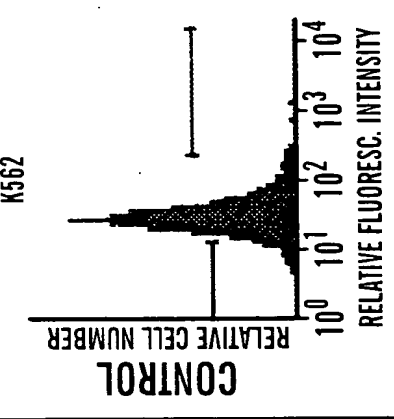
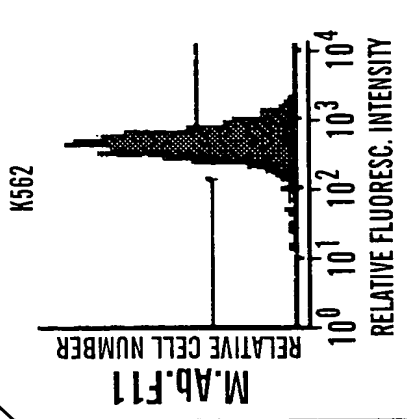


FIG. 7D

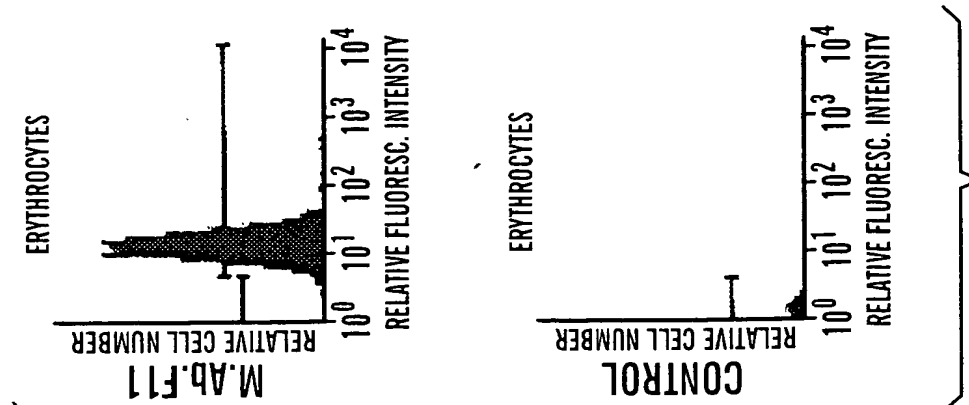


FIG. 7E

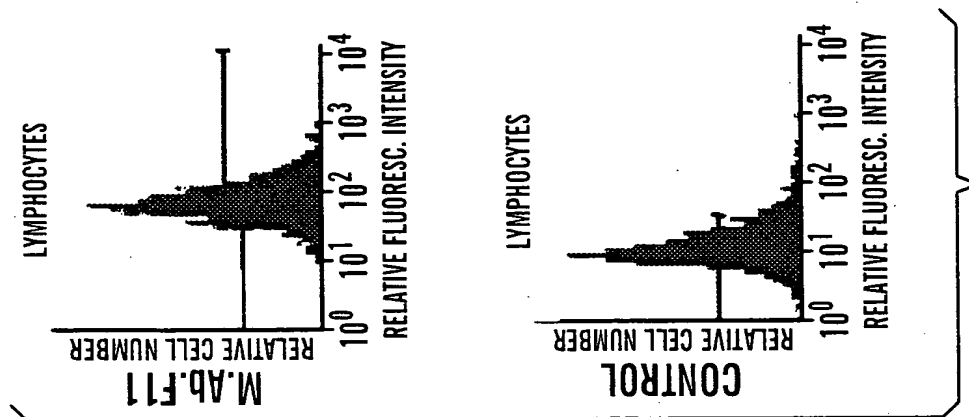


FIG. 7F

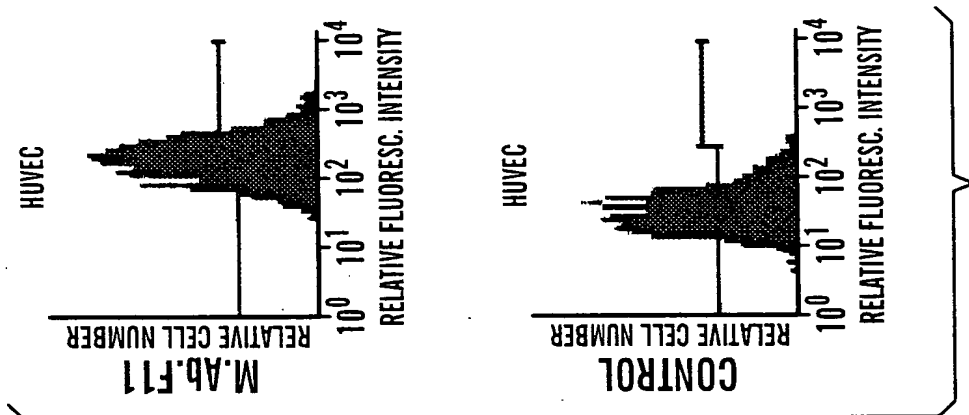


FIG. 7G

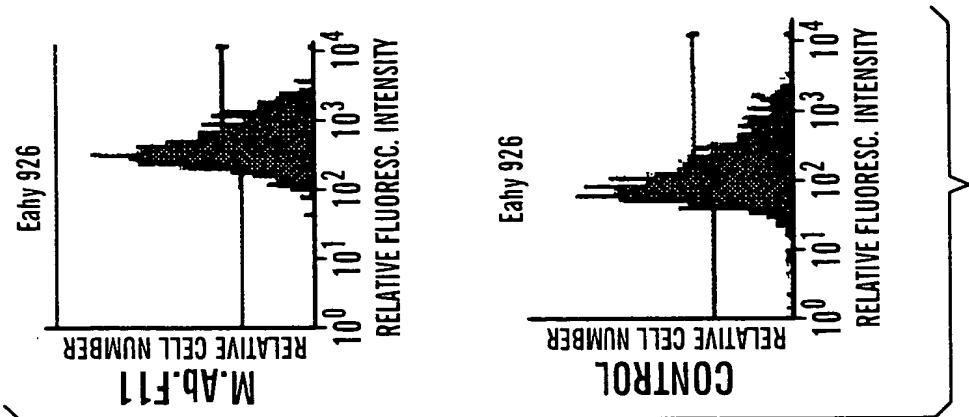


FIG. 7H

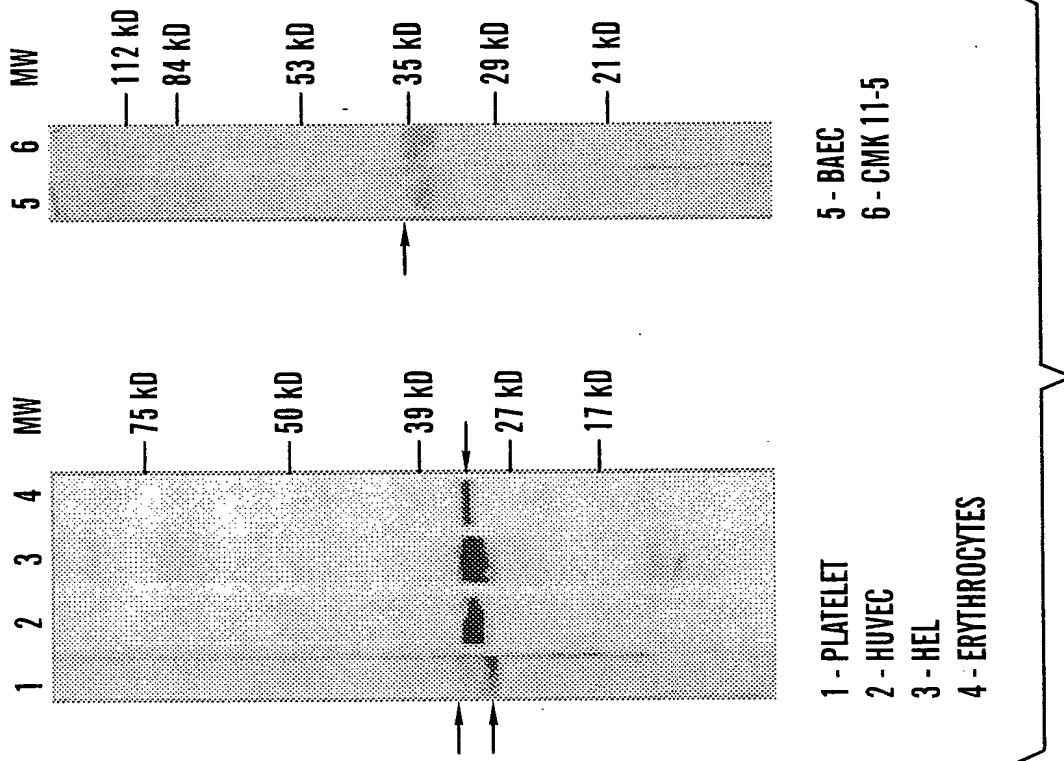


FIG. 7I

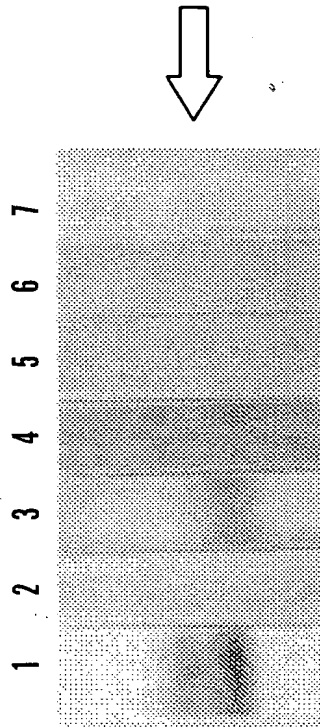


FIG. 8